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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

No statistical methods were used to pre-determine the sample size, but the sample size used in this study (n = 23) is comparable with previous fMRI studies using a similar paradigm (e.g., McNamee et al., Nat. Neuro, 2013; and Chib et al., JNS, 2009).

2. Data exclusions

Describe any data exclusions.

The data from one participant was excluded due to technical problems with the fMRI scanning.

3. Replication

Describe whether the experimental findings were reliably reproduced.

The value signals reported in the present manuscript have been reported in many previous studies. The findings about nutritive attributes were confirmed using multiple analytical approaches on the same data-set, showing robustness of our findings to different analytical methods. We have not re-run the study with another independent set of participants.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

In each of the run 1 and 3, randomly selected 28 out of the 56 food items were presented twice in random order (i.e., 56 trials for each run). The other 28 food items were presented twice in each of the run 2 and 4.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

No group allocation was used, and the investigators were not blinded to the conditions within participants -- it is not feasible to do so within the context of this experimental design.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	We used publicly available softwares: Psychtoolbox for stimulus presentations; and Matlab R2013b, SPM8 and The Decoding Toolbox (Hebart et al., 2015) for data analyses.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	N/A

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	N/A

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	N/A
b. Describe the method of cell line authentication used.	*Describe the authentication procedures for each cell line used OR declare that none of the cell lines used have been authenticated OR state that no eukaryotic cell lines were used.*
c. Report whether the cell lines were tested for mycoplasma contamination.	*Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination OR state that no eukaryotic cell lines were used.*
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	*Provide a rationale for the use of commonly misidentified cell lines OR state that no commonly misidentified cell lines were used.*

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	N/A

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	We used the data from 23 participants (8 females; age, 30.7 ± 4.12 years, MEAN ± SD; and BMI, 23.51 ± 4.00, MEAN ± SD). All the participants were preassessed to exclude those with any previous history of neurological/psychiatric illness. We also confirmed that the participants were not on a diet or seeking to lose weight for any reason.

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MRI Studies Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Experimental design

1. Describe the experimental design.	Task; event-related design
2. Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.	The task consists of 4 fMRI runs of the 56 trials (each trial takes 12s on average; and intervals between trials are jittered (2-12s)).
3. Describe how behavioral performance was measured.	Subjective values for food items were recorded.

Acquisition

4. Imaging	
a. Specify the type(s) of imaging.	Functional
b. Specify the field strength (in Tesla).	3T
c. Provide the essential sequence imaging parameters.	We used a one-shot T2*-weighted echo planar imaging sequence (Volume TR = 2780 ms, TE = 30 ms, FA = 80°). 44 oblique slices (thickness = 3.0 mm, gap = 0 mm, FOV = 192 × 192 mm, matrix = 64 × 64) were acquired per volume. The slices were aligned 30° to the AC–PC plane to reduce signal dropout in the orbitofrontal area.
d. For diffusion MRI, provide full details of imaging parameters.	N/A
5. State area of acquisition.	Whole-brain

Preprocessing

6. Describe the software used for preprocessing.	SPM8 on MATLAB R2013b
7. Normalization	
a. If data were normalized/standardized, describe the approach(es).	The standard procedure with segmentation in SPM8 was used.
b. Describe the template used for normalization/ transformation.	MNI template
8. Describe your procedure for artifact and structured noise removal.	Motion-correction parameters were included into the GLM.
9. Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.	We discarded volumes recorded at 10 sec and later from the end of the last trial in each run.

Statistical modeling & inference

10. Define your model type and settings.	Multi-voxel pattern analysis at the first-level; and random-effect analysis at the second-level

11. Specify the precise effect tested.	Mean value of the decoding accuracies over the participants
12. Analysis	
a. Specify whether analysis is whole brain or ROI-based.	We employed both whole-brain and ROI-based analyses.
b. If ROI-based, describe how anatomical locations were determined.	We used AAL database (Tzourio-Mazoyer et al., 2002).
13. State the statistic type for inference. (See Eklund et al. 2016.)	For the whole-brain analysis, we employed a cluster-level correction for multiple comparisons implemented in SPM8 (cluster-forming threshold P = 0.001).
14. Describe the type of correction and how it is obtained for multiple comparisons.	FWE
15. Connectivity	
a. For functional and/or effective connectivity, report the measures of dependence used and the model details.	Regression coefficient of the psycho-physiological Interaction term.
b. For graph analysis, report the dependent variable and functional connectivity measure.	N/A
16. For multivariate modeling and predictive analysis, specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.	Independent variables (classification samples) were voxel-wise fMRI responses to each food item; and the classification accuracy was evaluated by leave-one-run-out cross-validation.